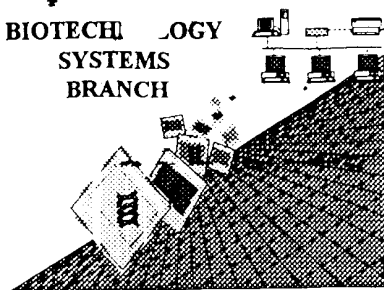


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Tanner

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RECEIVED

TECH CENTER 167

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/613,355A

Source: 1647

Date Processed by STIC: 11/27/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

#6

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/613,355A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

FYI

ED

[illegible]

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$$\begin{aligned}
 \mathcal{L}_1 &= \frac{1}{2} \|\mathbf{y} - \mathbf{A}\mathbf{x}\|_2^2 \\
 \mathcal{L}_2 &= \frac{1}{2} \|\mathbf{y} - \mathbf{A}\mathbf{x}\|_2^2 + \frac{\lambda}{2} \|\mathbf{x}\|_2^2 \\
 \mathcal{L}_3 &= \frac{1}{2} \|\mathbf{y} - \mathbf{A}\mathbf{x}\|_2^2 + \frac{\lambda}{2} \|\mathbf{x}\|_2^2 + \frac{\lambda}{2} \|\mathbf{x}\|_1 \\
 \mathcal{L}_4 &= \frac{1}{2} \|\mathbf{y} - \mathbf{A}\mathbf{x}\|_2^2 + \frac{\lambda}{2} \|\mathbf{x}\|_2^2 + \frac{\lambda}{2} \|\mathbf{x}\|_1 + \frac{\lambda}{2} \|\mathbf{x}\|_0
 \end{aligned}$$

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→ delete, if no response shown

Die abstrakte Variable  $\text{Hilf}$  wird durch die  
deletzte  $\emptyset \rightarrow 10$   
Hilf = Null; die Abstraktion von  $\text{Hilf} := 10$   
wird durch  $\text{Hilf} := 10$  dargestellt.  
Es ist also kein Wert für  $\text{Hilf}$  angegeben.  
Dieser Wert ist der Wert der Variablen  $\text{Hilf}$ .  
Der Wert der Variable  $\text{Hilf}$  ist 10.

29/6/13, 355A

2

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TECH CENTER 1600/2900

Per 1.824(a)(1) of new Sequence Rules:

"The computer readable form shall contain a single 'Sequence Listing'..."

DO NOT submit separate CRF's for each  
sequence

Sequence 2 follows Sequence 1 in  
one file

09/613,355A 3

~~SEQUENCE LISTING~~

<110> LIPPS, BINIE V.  
LIPPS, FREDERICK W.  
<120> SYNTHETIC PEPTIDE FOR NEUROLOGICAL DISORDERS  
<130> FWLPAT013US  
<140> US 09/613,355  
<141> 2000-07-11  
<150>  
<151>  
<160> 4  
<170> WORDPERFECT 5.1 FOR WINDOWS

<210> 2  
<211> ~~LENGTH:~~ 15

<212> PRT  
<213> SYNTHETIC

<400> 2

Asn Leu Gly Glu His Pro Val Cys Asp Ser Thr Asp Thr Trp Val  
5 10 15

Numerical identifiers  
<1107 through <1707  
appear once, at  
beginning of the  
Sequence Listing.

per new Sequence Rules, the only valid responses  
are: Unknown,

Artificial Sequence,  
or scientific  
name  
(Genus/species)

see item 12  
on Enr Summary  
sheet

Sequence 3 follows  
Sequence 2

09/613,355A 4

~~SEQUENCE LISTING~~

<110> LIPPS, BINIE V.  
LIPPS, FREDERICK W.

<120> SYNTHETIC PEPTIDE FOR NEUROLOGICAL DISORDERS

<130> FWLPAT013US

<140> US 09/613,355

<141> 2000-07-11

<150>  
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<160> 4

<170> WORDPERFECT 5.1 FOR WINDOWS

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<212> PRT

<213> SYNTHETIC

<400> 3

*see item 12 on Enr Summary Sheet*

Asn Leu Gly Glu His Pro Val Cys Asp Ser  
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*Seq. 4 follows*

~~SEQUENCE LISTING~~

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 <212> PRT  
 <213> SYNTHETIC  
 <400> 4

Asn Leu Gly Glu His  
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1) See sample Sequence Listing  
(attached) for valid format

2) Consult new Sequence Rules

FYI:

Please review the

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Appendix A To Subpart C to Part 1—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

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<140> US 08/999,999

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<150> EP 91000000

<151> 1997-12-31



<160> 2

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<213> Paramecium aurelia

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<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

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&lt;305&gt; 4

&lt;306&gt; 1 - 7

&lt;307&gt; 1988-06-20

&lt;400&gt; 1

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ctgactgact ctgagatagt cgagcccgta cgagaccctg cgaggggtgac agagagtggg 180

cgcggtgcgcg cagagcgccg cgccggtgcg cgcgcgagtg cgcggtgggc cgcgcgaggg 240

ctttegeggc agcgggcgcg ctttccggcg cgcgcccgtc cgccctaga cctgagaggt 300

cttctcttcc ctctcttcca ctgagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgtttgctc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

- 10

15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

ant Secretary of Commerce and  
issioner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

1 CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names, and/or Initials.	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212> Type

Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.

M

<213> Organism

Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.

M

<220> Feature

Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.

<221> Name/Key

Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence

<222> Location

Specify location within sequence; where appropriate state number of first and last bases/amino acids

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

<223>

Other Information

in feature

Other relevant information;  
four lines maximum

base was used in a sequence

M, under the following conditions:  
if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.

<300>

Publication Information

Leave blank after <300>

0

<301>

Authors

Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials

0

<302>

Title

0

<303>

Journal

0

<304>

Volume

0

<305>

Issue

0

<306>

Pages

0

<307>

Date

Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy

0

<308>

Database Accession Number

Accession number assigned by database including database name

0

<309>

Database Entry Date

Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy

0

<310>

Patent Document Number

Document number; for patent-type citations only. Specify as, for example, US 07/999,999

0

<311> Patent Filing  
Date

Document filing  
date, for patent-  
type citations only;  
specify as yyyy-mm-dd

<312> Publication Date

Document publication  
date, for  
patent-type  
citations only;  
specify as yyyy-mm-dd

<313> Relevant  
Residues

FROM (position) TO  
(position)

<400> Sequence

SEQ ID NO should  
follow the  
numeric identifier  
and should appear  
on the line pre-  
ceding the actual  
sequence

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;